

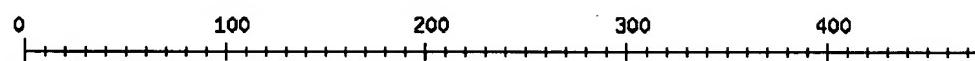
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i Release2005.1

Proteins sharing a prodom "Domain" with Q93GI2_MORBO (Q93GI2)



Complete output

 SEARCH|◀◀◀◀▶▶▶| [\[new window\]](#) [\[close\]](#)

	Q84C02_ACTPL	
	Q8KWZ6_ACTEU	
	Q47461_ECOLI	
	Q8GA40_ECOLI	
	Q93NP0_ACTPL	
	LKTA_ACTAC	
	Q43892_ACTAC	
	Q9L469_BORPA	
	Q7W1N2_BORPA	
	CYAA_BORPE	
	CYAA_BORBR	
	LKTA_PASSP	
	LKA3_PASHA	
	Q93GI2_MORBO	
	Q8KWZ9_BBBBB	
	Q93NP2_ACTPL	

Am. J. Vet. Res., 50:1437-1441.

Other Reference Publication (18):

Riley, Growth Requirements for Moraxella Bovis, Veterinary Microbiology, 9 (1984) 593-598.

Other Reference Publication (19):

Ostle et al., Outer Membrane Protein Antigens of Moraxella Bovis, Am. J. Vet. Res., vol. 47, No. 7, Jul., 1986.

CLAIMS:

1. A method of producing a M bovis cell culture comprising the steps of inoculating a colony of M bovis in a growth medium and causing said colony to grow therein and express outer membrane proteins, said medium having a low available iron content resulting in at least about 0.01% by weight of the total expressed outer membrane protein content having a molecular weight of about 104 kDa, as determined by sodium dodecyl sulfate polyacrylamide gel electrophoresis and quantified by soft laser densitometry.
5. A mixture of isolated outer membrane proteins derived from M bovis, said mixture including an outer membrane protein having a molecular weight of about 104 kDa, as determined by sodium dodecyl sulfate polyacrylamide gel electrophoresis.
9. An isolated outer membrane protein derived from M. bovis and having a molecular weight of about 104 kDa.

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WEST Search History

DATE: Thursday, April 06, 2006

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR</i>			
<input type="checkbox"/>	L1	epp and bovis	17
<input type="checkbox"/>	L2	39218 and bovis	1

END OF SEARCH HISTORY

WEST Search History

[Hide Items](#) [Restore](#) [Clear](#) [Cancel](#)

DATE: Thursday, April 06, 2006

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR</i>			
<input type="checkbox"/>	L1	leukotox\$ or leucotox\$ or leuco-tox\$ or leuko-tox\$	337
<input type="checkbox"/>	L2	fusion or fused or chimera or chimeric or heterologous or heter-ologous or foreign or subsequence or sub-sequence or single-chain or singlechain or pt7-7 or pproexhta or ppro or exhta	1563431
<input type="checkbox"/>	L3	hishishis or hishishishis or hishishishishis or hishishishishis or 6his or 6-his or 6xhis or 6x-his or polyhistidine or poly-his or 6histidine or poly6his or poly- 6his or nickel or chélate or metal	4592792
<input type="checkbox"/>	L4	L3 and l2 and l1	106
<input type="checkbox"/>	L5	L3.clm. and l2.clm. and l1.clm.	0
<input type="checkbox"/>	L6	L3.clm. and l1.clm.	0
<input type="checkbox"/>	L7	L3.clm. and l2.clm.	10305
<input type="checkbox"/>	L8	L7 and l1	1
<input type="checkbox"/>	L9	l1.clm.	51
<input type="checkbox"/>	L10	L9 and l3	9
<input type="checkbox"/>	L11	l1 near100 (epitope or fragment or segment or portion or subunit or sub-unit or truncate or truncated)	77
<input type="checkbox"/>	L12	L11 near100 (l3 or poly-hisitide or ninta or ni-nta)	3
<input type="checkbox"/>	L13	L11 and (l3 or poly-hisitide or ninta or ni-nta)	16
<input type="checkbox"/>	L14	L13 not l12	13
<input type="checkbox"/>	L15	(6797272 or 6096320 or 5837268 or 5594107).pn.	8
<input type="checkbox"/>	L16	('5594107' '6797272' '5837268' '6096320')!.ABPN1,NRPN,PN,TBAN,WKU.	8

END OF SEARCH HISTORY

Search Results - Record(s) 1 through 8 of 8 returned.

L16: Entry 1 of 8

File: USPT

Sep 28, 2004

US-PAT-NO: 6797272

DOCUMENT-IDENTIFIER: US 6797272 B1

TITLE: Enhanced immunogenicity using leukotoxin chimeras

DATE-ISSUED: September 28, 2004

US-CL-ISSUED: 424/192.1; 424/255.1, 424/185.1, 424/193.1, 424/195.11, 424/236.1,
424/241.1, 530/350, 530/351US-CL-CURRENT: 424/192.1; 424/185.1, 424/193.1, 424/195.11, 424/236.1, 424/241.1,
424/255.1, 530/350, 530/351INT-CL-ISSUED: [07] A61 K 39/00

L16: Entry 2 of 8

File: USPT

Aug 1, 2000

US-PAT-NO: 6096320

DOCUMENT-IDENTIFIER: US 6096320 A

TITLE: Vaccines with chimeric protein comprising gamma-interferon and leukotoxin
derived from pasteurella haemolytica

DATE-ISSUED: August 1, 2000

US-CL-ISSUED: 424/255.1; 424/192.1, 424/193.1, 424/195.11, 424/85.1, 424/85.4,
424/85.5, 435/69.5, 435/69.7, 530/350, 530/351US-CL-CURRENT: 424/255.1; 424/192.1, 424/193.1, 424/195.11, 424/85.1, 424/85.4,
424/85.5, 435/69.5, 435/69.7, 530/350, 530/351INT-CL-ISSUED: [07] A61 K 39/102

L16: Entry 3 of 8

File: USPT

Nov 17, 1998

US-PAT-NO: 5837268

DOCUMENT-IDENTIFIER: US 5837268 A

TITLE: GnRH-leukotoxin chimeras

DATE-ISSUED: November 17, 1998

US-CL-ISSUED: 424/255.1; 424/184.1, 424/200.1, 424/198.1, 424/193.1, 424/192.1,
530/300, 530/350, 514/2, 514/7, 514/12, 514/15, 935/11, 935/12, 935/13US-CL-CURRENT: 424/255.1; 424/184.1, 424/192.1, 424/193.1, 424/198.1, 424/200.1,
514/12, 514/15, 514/2, 514/7, 530/300, 530/350

INT-CL-ISSUED: [06] A61 K 38/00, A61 K 39/02, C12 N 15/00, C07 K 2/00

L16: Entry 4 of 8

File: USPT

Jan 14, 1997

US-PAT-NO: 5594107

DOCUMENT-IDENTIFIER: US 5594107 A

** See image for Certificate of Correction **

TITLE: Chimeric protein comprising an RTX-family cytotoxin and interferon-2 or interferon

DATE-ISSUED: January 14, 1997

US-CL-ISSUED: 530/350; 435/69.5, 435/69.7, 530/351, 530/825, 424/192.1, 424/195.11, 424/197.11, 424/85.1

US-CL-CURRENT: 530/350; 424/192.1, 424/195.11, 424/197.11, 424/85.1, 435/69.5, 435/69.7, 530/351, 530/825

INT-CL-ISSUED: [06] C12 N 15/19, A61 K 39/102

L16: Entry 5 of 8

File: DWPI

Aug 1, 2000

DERWENT-ACC-NO: 2000-531543

ABSTRACTED-PUB-NO: US 6096320A

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TITLE: Vaccine for stimulating immunity against pneumonia comprises chimeric protein comprising gamma-interferon and leukotoxin derived from Pasteurella haemolytica

INT-CL (IPC) : A61 K 39/102

Derwent-CL (DC) : B04, C06 , D16

CPI Codes: B04-H03F; B04-H05C; B04-N04; B14-S11; C04-H03F; C04-H05C; C04-N04; C14-S11; D05-H07; D05-H17C;

L16: Entry 6 of 8

File: DWPI

Mar 1, 2006

DERWENT-ACC-NO: 1998-159540

ABSTRACTED-PUB-NO: US 5837268A

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TITLE: Chimeric protein of leukotoxin and gonadotropin releasing hormone - useful for, e.g. preparation of vaccines for reduction of incidence of mammary tumours in mammals , US 6521746 B1

INT-CL (IPC) : A61 K 38/00, A61 K 38/09, A61 K 39/00, A61 K 39/02, A61 K 39/385, A61 K 39/39, A61 P 15/18, A61 P 35/00, C07 H 2/02, C07 H 2/04, C07 H 21/02, C07 H 21/04, C07 K 2/00, C07 K 7/23, C07 K 14/285, C07 K 14/575, C07 K 19/00, C12 N 0/00, C12 N 1/21, C12 N 15/00, C12 N 15/09, C12 N 15/16, C12 N 15/31, C12 N 15/62, C12 P 21/02, C12 P 21/04, C12 P 21/06, C12 N 1/21, C12 P 21/02, C12 R 1:19, C12 R 1:19

Derwent-CL (DC) : B04, D16

CPI Codes: B04-G01; B04-J07; B14-H01B; B14-S11C; D05-H07; D05-H12C; D05-H12E; D05-H17C;

L16: Entry 7 of 8

File: DWPI

Jan 14, 1997

DERWENT-ACC-NO: 1997-099529
ABSTRACTED-PUB-NO: US 5594107A
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TITLE: Immunogenic chimeric proteins comprising cytokine linked to RTX toxin - useful in vaccines, esp. against shipping fever in cattle

INT-CL (IPC): A61 K 39/102, C12 N 15/19

Derwent-CL (DC): B04, C06, D16

CPI Codes: B04-C01G; C04-C01G; B04-N02A; C04-N02A; B04-N03A; C04-N03A; B14-S11A; C14-S11A; D05-H07; D05-H17C; D05-H17C1;

L16: Entry 8 of 8

File: DWPI

Sep 28, 2004

DERWENT-ACC-NO: 1993-152482
ABSTRACTED-PUB-NO: US 5422110A
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TITLE: Immunological carrier system with enhanced immunogenicity - comprises chimeric protein comprising leuco:toxin peptide or homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone

INT-CL (IPC): A61 K 39/00, A61 K 39/02, A61 K 39/102, A61 K 39/15, C07 H 2/02, C07 H 2/04, C07 K 13/00, C12 N 15/31, C12 N 15/62, C12 P 21/06

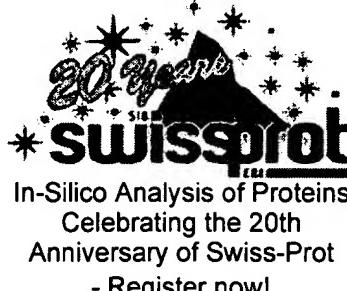
Derwent-CL (DC): B04, D16

CPI Codes: B02-V02; B04-B02B4; B04-B02D4; B04-B04A1; B04-B04A5; B04-C01; D05-C12; D05-H03B; D05-H07; D05-H10; D05-H12;

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UniProtKB/Swiss-Prot entry Q44066



[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#)
[\[Keywords\]](#) [\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	HLYA_AERHY
Primary accession number	Q44066
Secondary accession numbers	None
Integrated into Swiss-Prot on	June 1, 2001
Sequence was last modified on	November 1, 1996 (Sequence version 1)
Annotations were last modified on	February 7, 2006 (Entry version 30)

Name and origin of the protein

Protein name	Putative alpha-hemolysin
Synonyms	None
Gene name	Name: hlyA
From	Aeromonas hydrophila [TaxID: 644]
Taxonomy	Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales; Aeromonadaceae; Aeromonas.

References

[1] NUCLEOTIDE SEQUENCE [GENOMIC DNA].

STRAIN=Ah20;
 Chen J.D., Lai S.Y., Chen C.H.;
 "Cloning, expression and sequencing of Aeromonas hydrophila alpha-hemolysin gene determinant.";
 Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.

Comments

- **FUNCTION:** Lyses fish blood cells (*Potential*).
- **SIMILARITY:** Belongs to the UPF0161 family [view classification].

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Cross-references

Sequence databases

EMBL L36462; AAB81225.1; -;
Genomic_DNA. [EMBL / GenBank / DDBJ]
[CoDingSequence]

3D structure databases

ModBase Q44066.

Protein-protein interaction databases

DIP Q44066.

2D gel databases

SWISS-
2DPAGE Get region on 2D PAGE.

Organism-specific gene databases

HOGENOM [Family / Alignment / Tree]

Family and domain databases

HAMAP MF_00386; -; 1.
PBIL [Family / Alignment / Tree]

InterPro IPR002696; DUF37.
Graphical view of domain structure.

Pfam PF01809; DUF37; 1.
Pfam graphical view of domain structure.

ProDom PD004225; DUF37; 1.
[Domain structure / List of seq. sharing at least 1 domain]

TIGRFAMs TIGR00278; DUF37; 1.

BLOCKS Q44066.

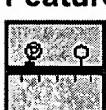
Other

ProtoNet Q44066.

UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

Cytolysis; Hemolysis; Toxin.

Features

Feature table viewer

Key	From	To	Length	Description	FTId
CHAIN	1	85	85	Putative alpha-hemolysin.	PRO_0000171785

Sequence information

Length: 85 AA [This is the length of the unprocessed precursor]

Molecular weight: 9345 Da
[This is the MW of the unprocessed precursor]

CRC64: 1FCEDA95833350C5
is a checksum on the sequence

10 20 30 40 50 60
MASALSPGSR VLIALIRVYQ RLISPLLGPH CRFTPTCSSY GIEALRRFGV IKGSWLTVKR

70 80
VLKCHPLHPG GDDPVPPGPF DTREH

Q
in
F/

for

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BLAST BLAST submission on
ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam,
ProtScale, Compute pI/Mw, PeptideMass,
PeptideCutter, Dotlet (Java)

proSite, ScanProsite, MotifScan



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SWISS-MODEL

NPS@ NPSA Sequence
analysis tools

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Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**

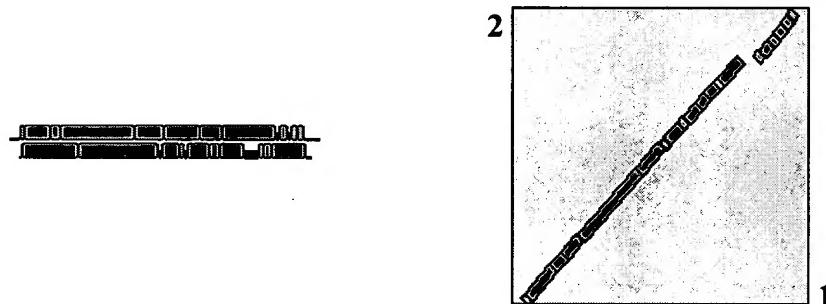
x_dropoff: **50** expect: **300.00** wordsize: **3** Filter View option **Standard**

Masking character option X for protein, n for nucleotide Masking color option **Black**

Show CDS translation Align

Sequence 1: gi|470685|gb|AAA21924.1|RTX toxin *lactococcus*
Length = 1049 (1 .. 1049)

Sequence 2: gi|15146408|gb|AAK84651.1|AF205359_1RTX toxin [Moraxella bovis]
Length = 927 (1 .. 927)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 714 bits (1843), Expect = 0.0
Identities = 425/970 (43%), Positives = 571/970 (58%), Gaps = 97/970 (10%)

Query 45	LAAGKAVQKYGNK-LVLVIPKEYDGSVGNNGFFDLVKAAEELGIQVKYVNRNELEVAHKSL	103
	+ AG K G K L L IPK+YD G D +KAA+ELGI N E A KS+	
Sbjct 11	IQAGLNSTKSGLKNLYLAIPKDYDPQKGCTLNDFIKADELGIARLAEPPNHTETAKKSV	70
Query 104	GTADQFLGLTERGLTFAPQLDQFLQKHSKISNVVGSSSTGDAVS-KLAKSQTIISGIQSV	162
	T +QFL LT+ G+ + A +L++FLQKHS G + + + KL K+ ++S + S	
Sbjct 71	DTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLKGASNVLSTLSSF	130
Query 163	LGTVLGINLNNEAIISGGSELE-LAEAGVSLASELVSNIAKGTTTIDAFTTQIQNFGKLA	221
	LGT LAGI L+ I G + + LA+A + L +E++ N+++ T TI+AF++Q+ G	
Sbjct 131	LGTALAGIELDSLICKGDAAPDALAKASIDLINIEIGNLSQSTQTIEAFSSLAKLGSTI	190
Query 222	ENAKGLGGVGRQLQNISGSALSKTGLGLDISSLLSGVTRSFALRNKNASTSTKVAAGFE	281
	AKG +G +LQN++ SKT LGL+II+ LLSG++ FAL +KNAST KVAAGFE	
Sbjct 191	SQAKGFSNIGNKLQNLN---FSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFE	247

Query	282	LSNQVIGGITKAVSSYILAQRRLAGLSTTGPAAALIASSISLAISPLAFLRVADNFNRSK	341
		LSNQVIG +TKA+SSY+LAQR+ AGLSTTG AALI SSI LAISPLAF+ AD FN +	
Sbjct	248	LSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVALITSSIMLAISPLAFMNAADKFHNHAN	307
Query	342	EIGEFAERFKKLGYDGDKLLSEFYHEAGTIDASITTISTALSAIAAGTAAASAGALVGAP	401
		+ EFA++F+K GYDGD LL+E+ GTI+AS+TTISTAL A++AG +AA+ G+ VGAP	
Sbjct	308	ALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTISTALGAVSAGVSAAVGSAVGAP	367
Query	402	ITLLVTGITGLISGILEFSKQPMLDHVASKIGNKIDEWEKKY-GKNYFENGYDARHKAFL	460
		I LLV G+TGLISGILE SKQ M + VA+++ KI EWEK+ G+NYF+ GYD+R+ A+L	
Sbjct	368	IALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGQNYFDKGYDSRYAAYL	427
Query	461	EDSFSLSSFNKQYETERAVLITQQRWDEYIGELAGITGKGDKLSSGKAYVDYFQEKGLL	520
		++ LS NK+ E ER + ITQQRWD IGELEGAT G+++ SGKAY D F++GK +	
Sbjct	428	ANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKV	487
Query	521	EKKPDDFSKVVFDPTKGEIDISNS--QTSTLLKFVTPLTPGTESRERTQTGKYEYITKL	578
		E S + D G IDISNS + + L F +PLLT GTESRER GKY YI KL	
Sbjct	488	EAG---SNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKSYINKL	543
Query	579	VVKGKDKWVWNGVKDKGAVYDYTNLIQHAHISSSVARGEEYREVRLVSHLGNGNDKVFLA	638
		W V + + D++ +IQ VA E E+ L+ + GND +F+	
Sbjct	544	KFGRVKNWQVTD-GEASSKLDPSKVIQR-----VAETEGTDEIGLIVNAKAGNDDIFVG	596
Query	639	AGSAEIHAGEGHDVYYDKT-DTGLLVIDGKATEQGRYSVTRELSGATKILREVIKNQK	697
		G I G+GHD V+Y K G + +DGT ATE G Y+V R+++ I EV+K Q+	
Sbjct	597	QGKMNIDGGDGHDVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARG-DIYHEVVKRQE	655
Query	698	YAVGKREETLEYRDYELTQSGNSNLKAHDELHSVEE-IGSNQRDEFKGSKFRDIFHGADG	756
		VGKR ET++YRDYEL + G ++ D L SVEE IGS D FKGSKF DIFH +G	
Sbjct	656	TKVGKRTETIQYRDYELRKVG-YGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSSEG	714
Query	757	DDLLNGNDGDDILYGDGNDELRGDNGNDQLYGGEGDDKLLGGNGNNYLGGDGNDLQV	816
		DDLL+G GDD L+G KGND L GD G+D L GG GDD L GG GN	
Sbjct	715	DDLDGGAGDDRLFGKGNDRLSGDEGDDLLGGSCDDVLNGGAGN-----	760
Query	817	LGNGFNVLGGKGDDKLYGSSGSDLLDGGEGLYLEGGDGSDFYVYRSTSGNHTIYDQGK	876
		D Y++R GN T+YD	
Sbjct	761	-----DVYIFRKGDGNDTLYD---	776
Query	877	ASDSDKLYLSDLSDFDNILVKRVNDNLEFRSNNNSNSGVLTIKDWFKGGNSYN-----H	929
		+ +DKL +D + +I+++R + + + N +SG + I W+ N N H	
Sbjct	777	GTGNDKLAFA DANISDI MIER TKEGIIVK--RNDHSGSINIPRWYITSNLQNYQSNKTDH	834
Query	930	KIEQIVDKNGRKLTAGNLGNNFHD---TQQASSLLKNVTQEQQNESNLSS--LKTELGKI	983
		KIEQ++ K+G +T+ + D T S LK + E LS+ + + L K+	
Sbjct	835	KIEQLIGKDGSYITSQIDKILQDKKDGTVITSQELKKLA DENKSQKLSASDIASSLNKL	894
Query	984	ITNAGNFGVA 993	
		+ + FG A	
Sbjct	895	VGSMALFGTA 904	

CPU time: 0.07 user secs. 0.01 sys. secs 0.08 total secs.

Lambda	K	H
0.311	0.131	0.361

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 9204

Number of extensions: 5598

Number of successful extensions: 52

Number of sequences better than 300.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 1049

Length of database: 1,215,510,009

Length adjustment: 144

Effective length of query: 905

Effective length of database: 1,215,509,865

Effective search space: 1100036427825

Effective search space used: 1100036427825

Neighboring words threshold: 9

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.8 bits)

S2: 71 (32.0 bits)

Entrez Protein

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PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Display **GenPept** Show 5

Range: from **begin** to **end** Features: SNP CDD MGC HPRD STS tRN

□ 1: BAA04014. Reports RTX toxin I type ...[gi:497787]

[BLink](#), [Conserved Domains](#), [Links](#)

<u>Comment</u>	<u>Features</u>	<u>Sequence</u>
LOCUS	BAA04014	1023 aa linear BCT 04-FEB-1999
DEFINITION	RTX toxin I type L [Actinobacillus pleuropneumoniae].	
ACCESSION	BAA04014	
VERSION	BAA04014.1 GI:497787	
DBSOURCE	locus ACNAPXIA accession <u>D16582.1</u>	
KEYWORDS	.	
SOURCE	Actinobacillus pleuropneumoniae	
ORGANISM	<u>Actinobacillus pleuropneumoniae</u> Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Actinobacillus.	
REFERENCE	1 (sites)	
AUTHORS	Frey,J., Meier,R., Gygi,D. and Nicolet,J.	
TITLE	Nucleotide sequence of the hemolysin I gene from <i>Actinobacillus pleuropneumoniae</i>	
JOURNAL	Infect. Immun. 59 (9), 3026-3032 (1991)	
PUBMED	<u>1879928</u>	
REFERENCE	2 (residues 1 to 1023)	
AUTHORS	Nagai,S., Yagihashi,T. and Ishihama,A.	
TITLE	DNA sequence analysis of an allelic variant of the <i>Actinobacillus pleuropneumoniae</i> -RTX-toxin I (ApxIA) from serotype 10	
JOURNAL	Microb. Pathog. 15 (6), 485-495 (1993)	
PUBMED	<u>8007819</u>	
REFERENCE	3 (residues 1 to 1023)	
AUTHORS	Nagai,S.	
TITLE	Direct Submission	
JOURNAL	Submitted (02-JUL-1993) Shinya Nagai, Nippon Institute of Biological Science; 2221-1, Shinmachi, Oume, Tokyo 198, Japan (E-mail:nfujita, Tel:0428-33-1037, Fax:0428-31-6166)	
COMMENT	Submitted (02-Jul-1993) to DDBJ by: Shinya Nagai Nippon Institute of Biological Science 2221-1 Shinmachi Oume, Tokyo 198 Japan Phone: 0428-33-1037 Fax: 0428-31-616.	
FEATURES	Location/Qualifiers	
source	1..1023 /organism="Actinobacillus pleuropneumoniae" /strain="13039" /db_xref="taxon:715"	

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 /region_name="RTX N-terminal domain"
 /note="RTX"
 /db_xref="CDD:8277"
Region <729..850
 /region_name="RTX toxins and related Ca2+-binding proteins
 [Secondary metabolites biosynthesis, transport, and
 catabolism]"
 /note="COG2931"
 /db_xref="CDD:12280"
CDS 1..1023
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 /coded_by="D16582.1:58..3129"
 /transl_table=11

ORIGIN

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1021 qsa
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Mar 14 2006 11:51:02

 NCBI	BLAST	Protein	Structure	PubMed	Taxonomy
	Genome	Nucleotide	3D-Domains	Books	Help

Query: gi|470685 RTX toxin

Matching gi: 1710800

COG2931 assigned by Cognitor (2 best hits)

200 BLAST hits to 53 unique species Sort by taxonomy proximity

0 Archaea 200 Bacteria 0 Metazoa 0 Fungi 0 Plants 0 Viruses 0 Other Eukaryotae

Keep only

 Cut-Off

New search by GI:

1049 aa

Conserved Domain Database hits					
SCORE	P	ACCESSION	GI	PROTEIN DESCRIPTION	
5074	9	P55131	1710801	RTX-III toxin determinant A	f
5052	9	AAK50053	13937109	RTX-toxin IIIA [Actinobacillu	
4502	7	Q9RCG8	73621356	Exotoxin paxA	
2644	5	CAD33759	24528030	hemolysin A [Escherichia coli	
2638	5	NP_755445	26249405	Hemolysin A [Escherichia coli	
2625	5	CAD42039	23954242	HlyA protein [Escherichia col	
2624	5	1208296B	225074	hemolysin hlyA	
2624	5	AAA23975	146379	chromosomal hemolysin A (hlyA	
2611	5	AAA98233	150682	hemolysin A [Escherichia coli	
2477	9	AAL55666	18026877	ApxIA [Actinobacillus pleurop	
2463	9	AAB17220	1477457	RTX-1 toxin determinant [Acti	
2462	9	ZP_001...	46143512	COG2931: RTX toxins and relat	
2442	9	P55128	1710793	RTX-I toxin determinant A fro	
2432	9	AAK50051	13937105	RTX toxin IA [Actinobacillus	
2432	9	P55129	1710794	RTX-I toxin determinant A fro	
2377	5	AAC24352	3253294	hemolysin [Escherichia coli]	
2375	5	YP_308794	73853298	Hemolysin A [Escherichia coli	
2369	5	BAA93708	7416116	hemolysin A [Escherichia coli	
2345	5	YP_325608	75994494	hemolysin toxin protein [Esch	
2340	5	CAA63849	1524027	EHEC-hemolysin [Escherichia c	
2327	5	CAA60042	1805762	EHEC-hlyA [Escherichia coli]	
2322	5	CAA56234	4388764	hemolysin [Escherichia coli]	
2213	8	CAA34731	38645	leukotoxin [Actinobacillus ac	
2168	8	AAA21922	141834	leukotoxin (Lta)	
2127	8	AAM45569	21305108	AqxA [Actinobacillus equuli]	
2123	8	AAM45566	21305104	AqxA [Actinobacillus cf. equu	
1981	5	AAA20544	525329	HlyA [Escherichia coli]	
1959	7	AAG40310	11762064	leukotoxin [Pasteurella treha	
1956	7	P55117	73620926	Leukotoxin (Lkt)	
1947	7	Q9ETX2	73621170	Leukotoxin (Lkt)	
1943	7	AAG40303	11762050	leukotoxin [Mannheimia glucos	
1941	7	AAR09165	38046598	leukotoxin structural protein	
1938	7	Q7BHI8	73621154	Leukotoxin (Lkt)	
1937	7	Q9EV34	73621169	Leukotoxin (Lkt)	
1937	7	AAG40300	11762044	leukotoxin [Mannheimia haemol	
1927	7	POC082	73621157	Leukotoxin (Lkt)	

		1925	8	AAX21415	60476777	ApxIIA [Actinobacillus porcit
		1920	7	CAA81206	400425	leukotoxin A [Mannheimia haem
		1919	9	AAU84700	52630374	ApxIIA [Actinobacillus pleuro
		1916	7	AAA25543	150513	leukotoxin membrane protein (
		1915	7	AAG40306	11762056	leukotoxin [Mannheimia glucos
		1914	8	A43834	285302	toxin II - Actinobacillus sui
		1912	7	AAG40304	11762052	leukotoxin [Mannheimia glucos
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		1911	7	POC085	73621161	Leukotoxin (Lkt)
		1911	7	Q9EV29	73621158	Leukotoxin (Lkt)
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		1903	7	Q9EV32	73621153	Leukotoxin (Lkt)
		1900	7	Q9EV30	73621155	Leukotoxin (Lkt)
		1898	9	AA074635	29470157	ApxIIA [Actinobacillus pleuro
		1898	7	P55123	1708221	Leukotoxin (PLkt)
		1898	9	ZP_001...	32035699	COG2931: RTX toxins and relat
		1897	9	AAK50052	13937107	RTX toxin IIA [Actinobacillus
		1896	8	Q00951	232261	Hemolysin (Cytolysin II) (CLY
		1893	7	AAB36691	397995	LktA
		1891	7	P55118	1708215	Leukotoxin (Lkt)
		1830	5	AAK84651	15146408	RTX toxin [Moraxella bovis]
		1749	5	ZP_007...	75234729	COG2931: RTX toxins and relat
		1494	7	AAR09161	38046593	leukotoxin structural protein
		1479	7	AAR09157	38046588	leukotoxin structural protein
		1142	9	CAB37652	4467352	apxIIIBD [Actinobacillus pleu
		1134	5	ZP_007...	75242313	COG2931: RTX toxins and relat
		861	5	AAR87855	40557139	HlyA [Escherichia coli]
		648	7	AAW21429	56681786	leukotoxin A [Pasteurellaceae]
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		633	7	AAW21425	56681778	leukotoxin A [Pasteurellaceae]
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		622	7	AAW21424	56681776	leukotoxin A [Pasteurellaceae]
		621	7	AAW21437	56681802	leukotoxin A [Pasteurellaceae]
		619	7	AAW21423	56681774	leukotoxin A [Pasteurellaceae]
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		606	4	Q57506	34978374	Bifunctional hemolysin-adenyl
		606	4	NP_886873	33599313	bifunctional hemolysin-adenyl
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		602	4	CAB76450	7160624	bifunctional hemolysin-adenyl
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		601	4	S51672	1073227	adenylate cyclase hemolysin -
		600	4	CAA68613	396666	unnamed protein product [Bord
		515	7	ABC16629	83356276	leukotoxin structural protein
		508	7	ABC16619	83356256	leukotoxin structural protein
		507	7	ABC16624	83356266	leukotoxin structural protein
		506	7	ABC16627	83356272	leukotoxin structural protein
		506	7	ABC16618	83356254	leukotoxin structural protein
		506	7	ABC16616	83356250	leukotoxin structural protein

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	<u>351</u>	<u>4</u>	<u>NP_274427</u>	<u>15677274</u>	iron-regulated protein FrpC [
	<u>342</u>	<u>3</u>	<u>ZP_005...</u>	<u>67938048</u>	Hemolysin-type calcium-bindin
	<u>342</u>	<u>4</u>	<u>P55127</u>	<u>1706913</u>	Iron-regulated protein frpC
	<u>341</u>	<u>5</u>	<u>YP_245455</u>	<u>66968578</u>	HlyJ haemolysin-like protein
	<u>341</u>	<u>4</u>	<u>AAD02003</u>	<u>4104348</u>	S-layer-RTX protein [Campylob
	<u>340</u>	<u>4</u>	<u>P55126</u>	<u>1706912</u>	Iron-regulated protein frpA
	<u>324</u>	<u>4</u>	<u>NP_518370</u>	<u>17544968</u>	PUTATIVE CALCIUM BINDING HEMO